```
      10                  30                  50
CGCCCAGCCGCCGCCTCCAAGCCCCTGAGGTTTCCGGGGACCACAATGAACAAGTTGCTG
                                                M  N  K  L  L
      70                  90                  110
TGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACCCAGGAAACGTTTCCT
C  C  A  L  V  F  L  D  I  S  I  K  W  T  T  Q  E  T  F  P
     130                 150                 170
CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCT
P  K  Y  L  H  Y  D  E  E  T  S  H  Q  L  L  C  D  K  C  P
     190                 210                 230
CCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC
P  G  T  Y  L  K  Q  H  C  T  A  K  W  K  T  V  C  A  P  C
     250                 270                 290
CCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATACTGCAGCCCC
P  D  H  Y  Y  T  D  S  W  H  T  S  D  E  C  L  Y  C  S  P
     310                 330                 350
GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGC
V  C  K  E  L  Q  Y  V  K  Q  E  C  N  R  T  H  N  R  V  C
     370                 390                 410
GAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCT
E  C  K  E  G  R  Y  L  E  I  E  F  C  L  K  H  R  S  C  P
     430                 450                 470
CCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACAGTTTGCAAAAGATGT
P  G  F  G  V  V  Q  A  G  T  P  E  R  N  T  V  C  K  R  C
     490                 510                 530
CCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGTAGAAAACACACAAAT
P  D  G  F  F  S  N  E  T  S  S  K  A  P  C  R  K  H  T  N
     550                 570                 590
TGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATATGT
C  S  V  F  G  L  L  L  T  Q  K  G  N  A  T  H  D  N  I  C
     610                 630                 650
TCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGTGAGGAGGCA
S  G  N  S  E  S  T  Q  K  C  G  I  D  V  T  L  C  E  E  A
     670                 690                 710
TTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAACTGGCTTAGTGTCTTGGTAGAC
F  F  R  F  A  V  P  T  K  F  T  P  N  W  L  S  V  L  V  D
     730                 750                 770
AATTTGCCTGGCACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAGC
N  L  P  G  T  K  V  N  A  E  S  V  E  R  I  K  R  Q  H  S
     790                 810                 830
TCACAAGAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCAAAACAAAGACCAAGAT
S  Q  E  Q  T  F  Q  L  L  K  L  W  K  H  Q  N  K  D  Q  D
     850                 870                 890
ATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGCGTGCAGCGGCACATT
I  V  K  K  I  I  Q  D  I  D  L  C  E  N  S  V  Q  R  H  I
     910                 930                 950
GGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAAGCTTACCGGGAAAG
G  H  A  N  L  T  F  E  Q  L  R  S  L  M  E  S  L  P  G  K
     970                 990                1010
AAAGTGGGAGCAGAAGACATTGAAAAAACAATAAAGGCATGCAAACCCAGTGACCAGATC
K  V  G  A  E  D  I  E  K  T  I  K  A  C  K  P  S  D  Q  I
    1030                1050                1070
CTGAAGCTGCTCAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTTGAAGGGCCTA
L  K  L  L  S  L  W  R  I  K  N  G  D  Q  D  T  L  K  G  L
    1090                1110                1130
ATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACTGTCACTCAGAGTCTA
```

FIGURE 1(A)

```
M  H  A  L  K  H  S  K  T  Y  H  F  P  K  T  V  T  Q  S  L
      1150                1170                1190
AAGAAGACCATCAGGTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTT
K  K  T  I  R  F  L  H  S  F  T  M  Y  K  L  Y  Q  K  L  F
      1210                1230                1250
TTAGAAATGATAGGTAACCAGGTCCAATCAGTAAAAATAAGCTGCTTATAACTGGAAATG
L  E  M  I  G  N  Q  V  Q  S  V  K  I  S  C  L  *
      1270                1290                1310
GCCATTGAGCTGTTTCCTCACAATTGGCGAGATCCCATGGATGAGTAAACTGTTTCTCAG
      1330                1350                1370
GCACTTGAGGCTTTCAGTGATATCTTTCTCATTACCAGTGACTAATTTTGCCACAGGGTA
      1390                1410                1430
CTAAAAGAAACTATGATGTGGAGAAAGGACTAACATCTCCTCCAATAAACCCCAAATGGT
      1450                1470                1490
TAATCCAACTGTCAGATCTGGATCGTTATCTACTGACTATATTTTCCCTTATTACTGCTT
      1510
GCAGTAATTCAACTGGAAAAAAAAAAA
```

FIGURE 1(B)

```
          10                  30                  50
ATGAACAAGTTGCTGTGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACC
M  N  K  L  L  C  C  A  L  V  F  L  D  I  S  I  K  W  T  T
          70                  90                  110
CAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG
Q  E  T  F  P  P  K  Y  L  H  Y  D  E  E  T  S  H  Q  L  L
         130                 150                 170
TGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACC
C  D  K  C  P  P  G  T  Y  L  K  Q  H  C  T  A  K  W  K  T
         190                 210                 230
GTGTGCGCCCCTTGCCCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGT
V  C  A  P  C  P  D  H  Y  Y  T  D  S  W  H  T  S  D  E  C
         250                 270                 290
CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC
L  Y  C  S  P  V  C  K  E  L  Q  Y  V  K  Q  E  C  N  R  T
         310                 330                 350
CACAACCGCGTGTGCGAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA
H  N  R  V  C  E  C  K  E  G  R  Y  L  E  I  E  F  C  L  K
         370                 390                 410
CATAGGAGCTGCCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACA
H  R  S  C  P  P  G  F  G  V  V  Q  A  G  T  P  E  R  N  T
         430                 450                 470
GTTTGCAAAAGATGTCCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGT
V  C  K  R  C  P  D  G  F  F  S  N  E  T  S  S  K  A  P  C
         490                 510                 530
AGAAAACACACAAATTGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACA
R  K  H  T  N  C  S  V  F  G  L  L  L  T  Q  K  G  N  A  T
         550                 570                 590
CACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACC
H  D  N  I  C  S  G  N  S  E  S  T  Q  K  C  G  I  D  V  T
         610                 630                 650
CTGTGTGAGGAGGCATTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAACTGGCTT
L  C  E  E  A  F  F  R  F  A  V  P  T  K  F  T  P  N  W  L
         670                 690                 710
AGTGTCTTGGTAGACAATTTGCCTGGCACCAAAGTAAACGCAGAGAGTGTAGAGAGGATA
S  V  L  V  D  N  L  P  G  T  K  V  N  A  E  S  V  E  R  I
         730                 750                 770
AAACGGCAACACAGCTCACAAGAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCAA
K  R  Q  H  S  S  Q  E  Q  T  F  Q  L  L  K  L  W  K  H  Q
         790                 810                 830
AACAAAGACCAAGATATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGC
N  K  D  Q  D  I  V  K  K  I  I  Q  D  I  D  L  C  E  N  S
         850                 870                 890
GTGCAGCGGCACATTGGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAA
V  Q  R  H  I  G  H  A  N  L  T  F  E  Q  L  R  S  L  M  E
         910                 930                 950
AGCTTACCGGGAAAGAAAGTGGGAGCAGAAGACATTGAAAAAACAATAAAGGCATGCAAA
S  L  P  G  K  K  V  G  A  E  D  I  E  K  T  I  K  A  C  K
         970                 990                1010
CCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGGCGAATAAAAAATGGCGACCAAGAC
P  S  D  Q  I  L  K  L  L  S  L  W  R  I  K  N  G  D  Q  D
        1030                1050                1070
ACCTTGAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACT
T  L  K  G  L  M  H  A  L  K  H  S  K  T  Y  H  F  P  K  T
        1090                1110                1130
GTCACTCAGAGTCTAAAGAAGACCATCAGGTTCCTTCACAGCTTCACAATGTACAAATTG
V  T  Q  S  L  K  K  T  I  R  F  L  H  S  F  T  M  Y  K  L
        1150                1170
```

FIGURE 2(A)

TATCAGAAGTTATTTTTAGAAATGATAGGTAATCTAGAAAAGATCTAA
Y Q K L F L E M I G N L E K I

FIGURE 2(B)

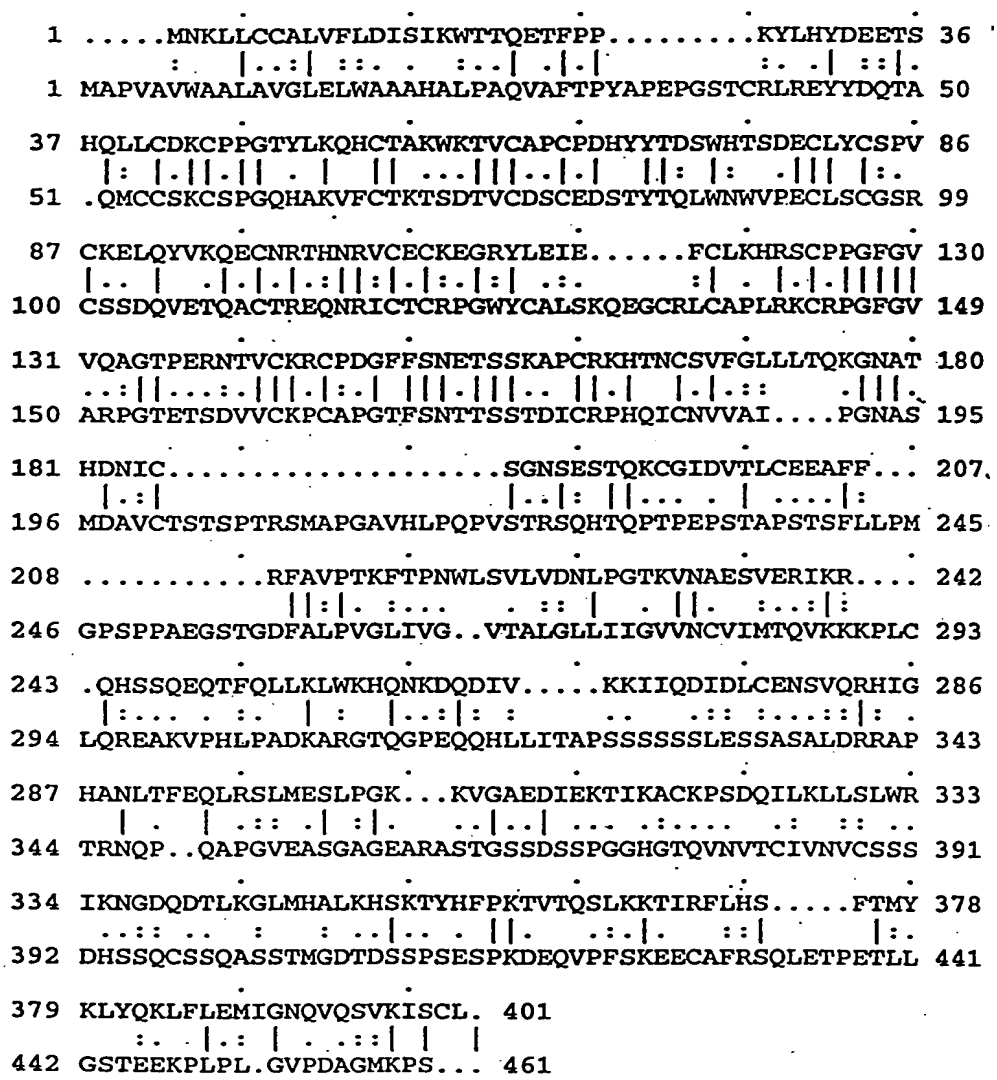

1 .....MNKLLCCALVFLDISIKWTTQETFPP.....KYLHYDEETS 36
1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTA 50
37 HQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPV 86
51 .QMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR 99
87 CKELQYVKQECNRTHNRVCECKEGRYLEIE.....FCLKHRSCPPGFGV 130
100 CSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGV 149
131 VQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180
150 ARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI....PGNAS 195
181 HDNIC.....SGNSESTQKCGIDVTLCEEAFF... 207
196 MDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPM 245
208 .....RFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKR.... 242
246 GPSPPAEGSTGDFALPVGLIVG..VTALGLLIIGVVNCVIMTQVKKKPLC 293
243 .QHSSQEQTFQLLKLWKHQNKDQDIV.....KKIIQDIDLCENSVQRHIG 286
294 LQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAP 343
287 HANLTFEQLRSLMESLPGK...KVGAEDIEKTIKACKPSDQILKLLSLWR 333
344 TRNQP..QAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSS 391
334 IKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHS.....FTMY 378
392 DHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLL 441
379 KLYQKLFLEMIGNQVQSVKISCL. 401
442 GSTEEKPLPL.GVPDAGMKPS... 461

FIGURE 3

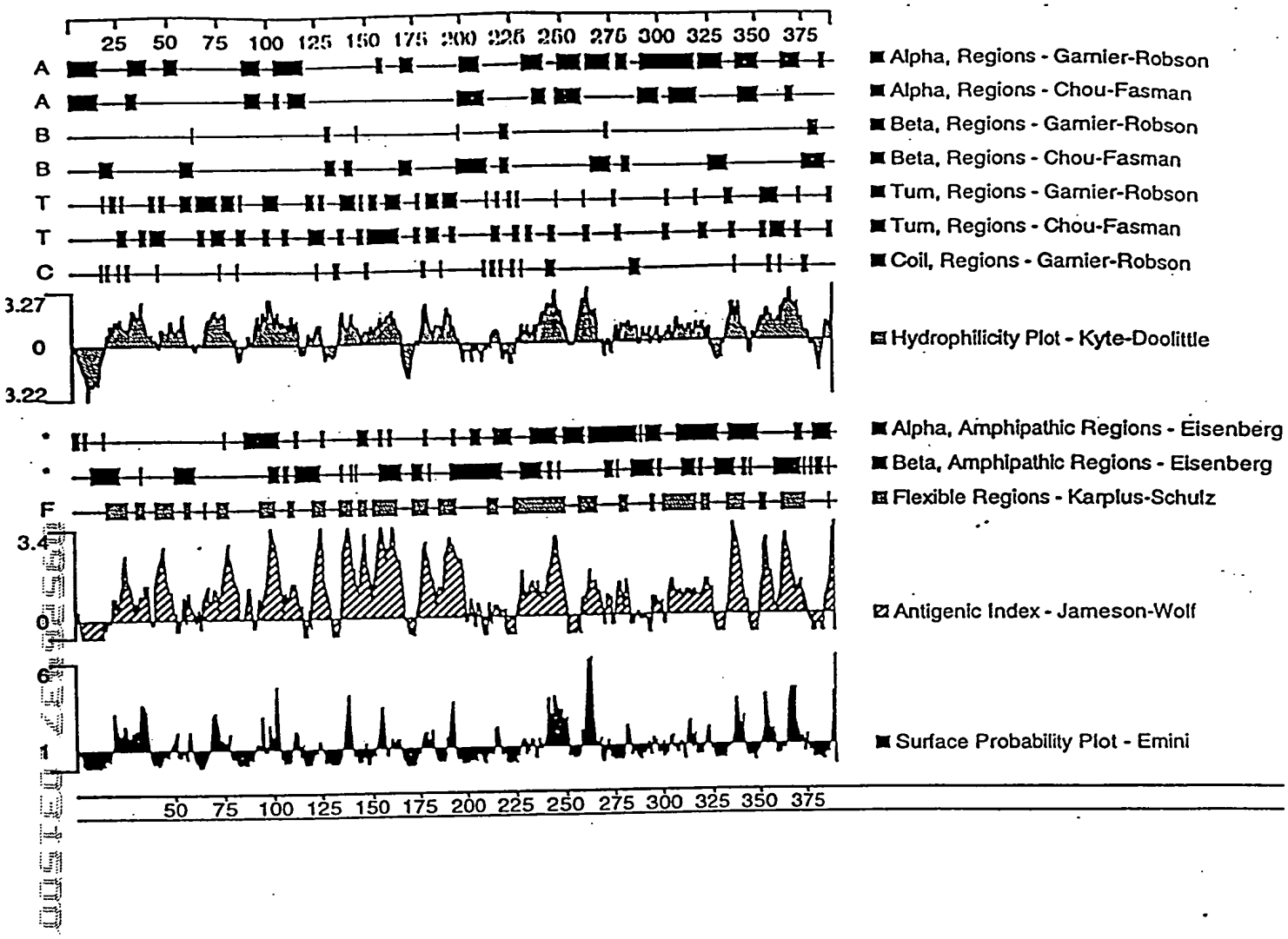

25 50 75 100 125 150 175 200 225 250 275 300 325 350 375
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
3.27
0
3.22
Hydrophilicity Plot - Kyte-Doolittle
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
50 75 100 125 150 175 200 225 250 275 300 325 350 375

FIGURE 4

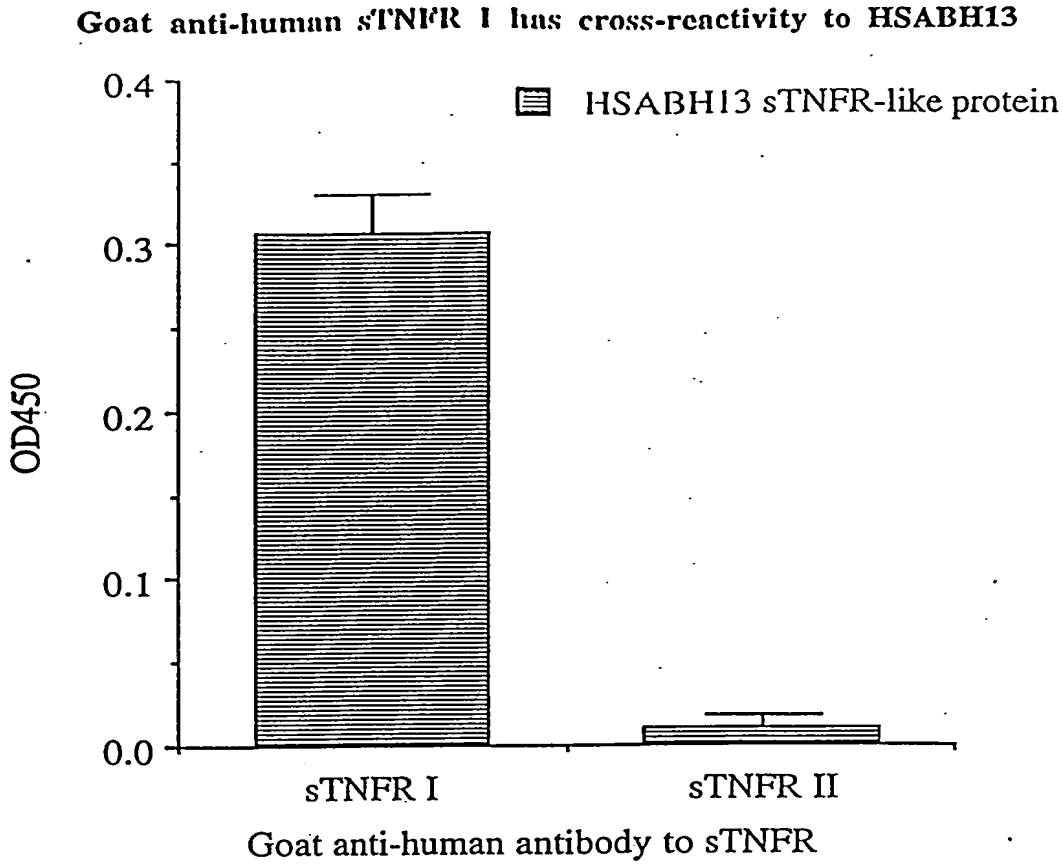
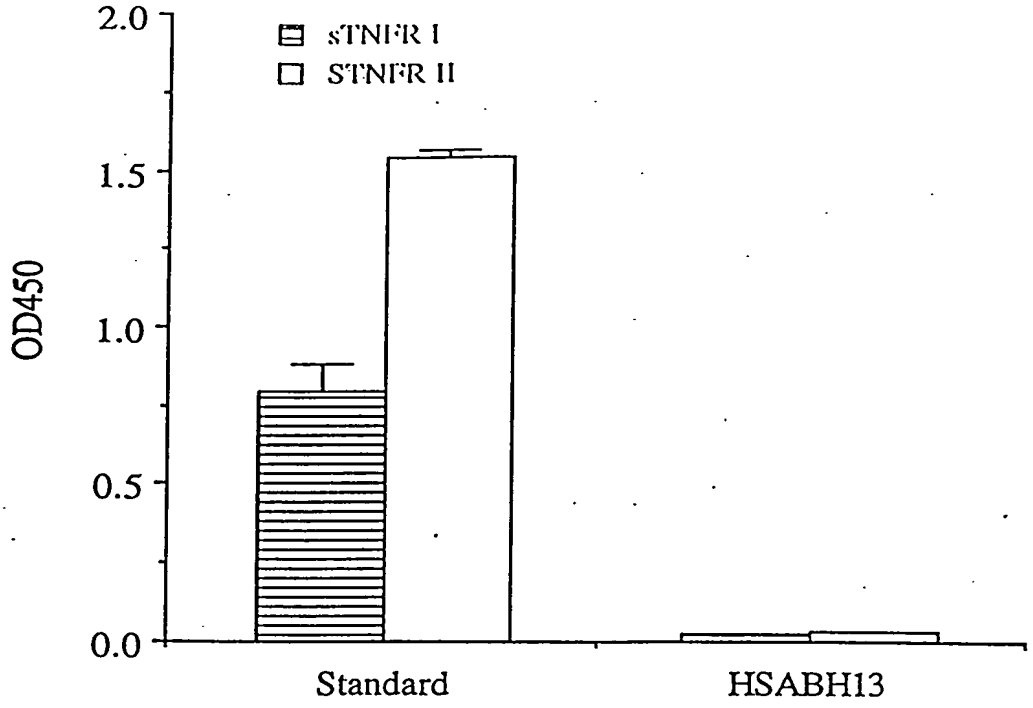

Goat anti-human sTNFR I has cross-reactivity to HSABH13
HSABH13 sTNFR-like protein
OD450
0.4
0.3
0.2
0.1
0.0
sTNFR I
sTNFR II
Goat anti-human antibody to sTNFR

FIGURE 5

HSABH13 does not bind to the mAb to sTNFR I or sTNFR II



ELISA Assay (plate coated with mAb to sTNFR I or STNFR II)

FIGURE 6

TNF-beta has higher affinty to HSAHAB13 than TNF-alpha, and HUVEO19 does not inhibit the binding

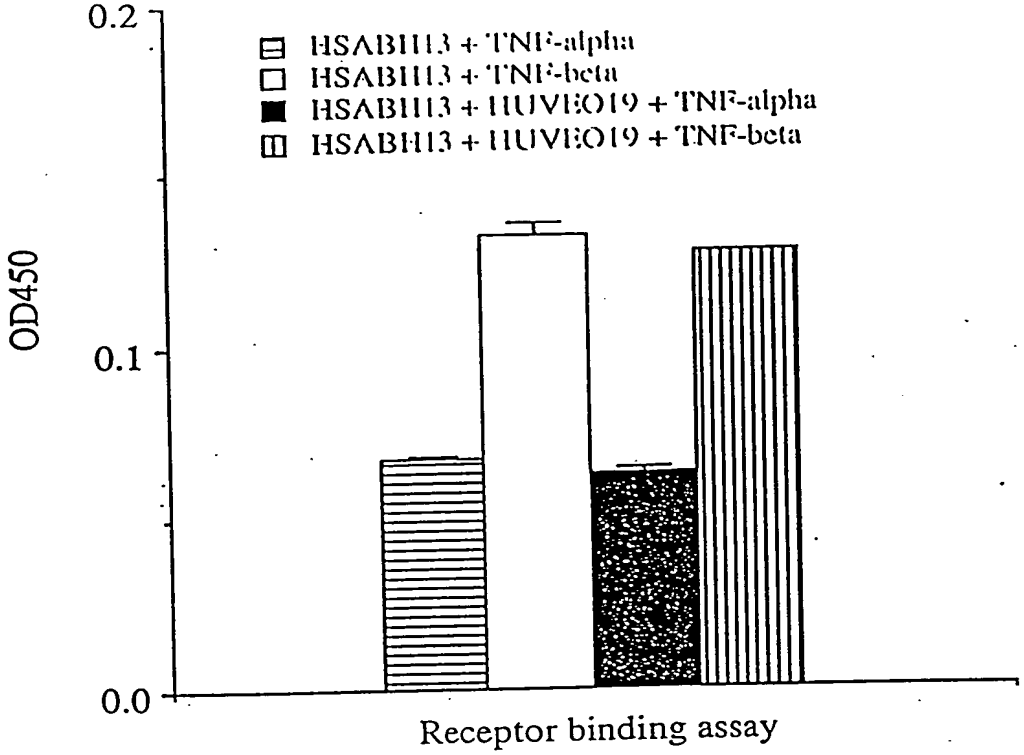


FIGURE 7

HSABH13 does not compete with sTNFR I to bind TNF-alpha, may compete with sTNFR II to bind TNF-alpha

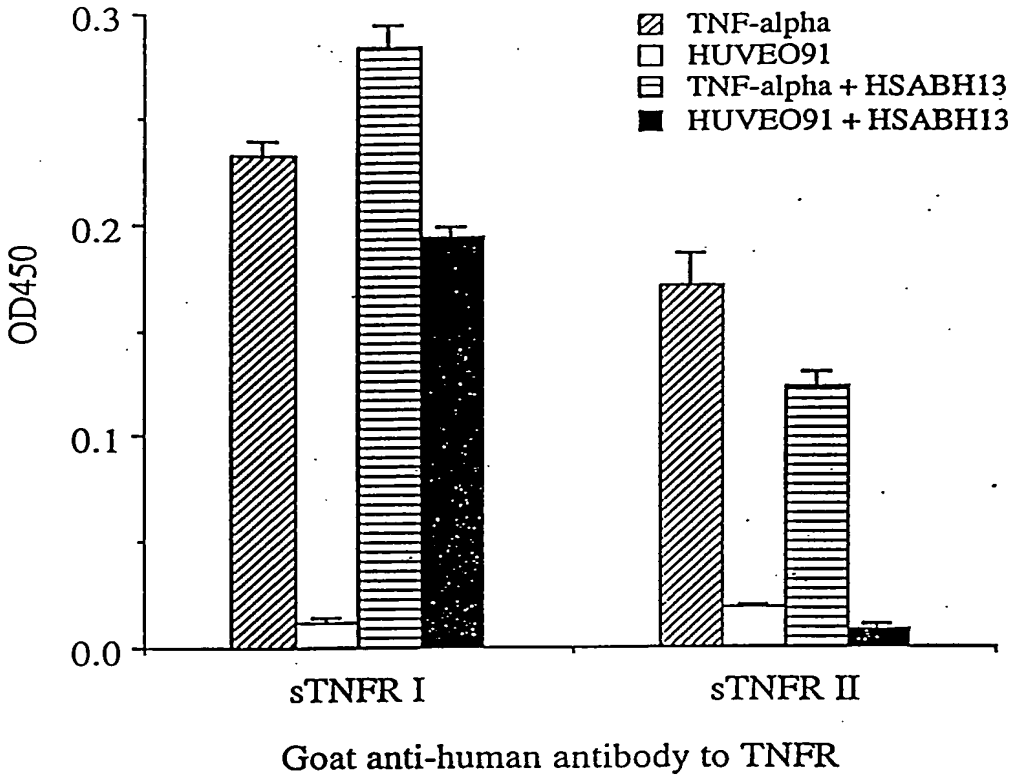
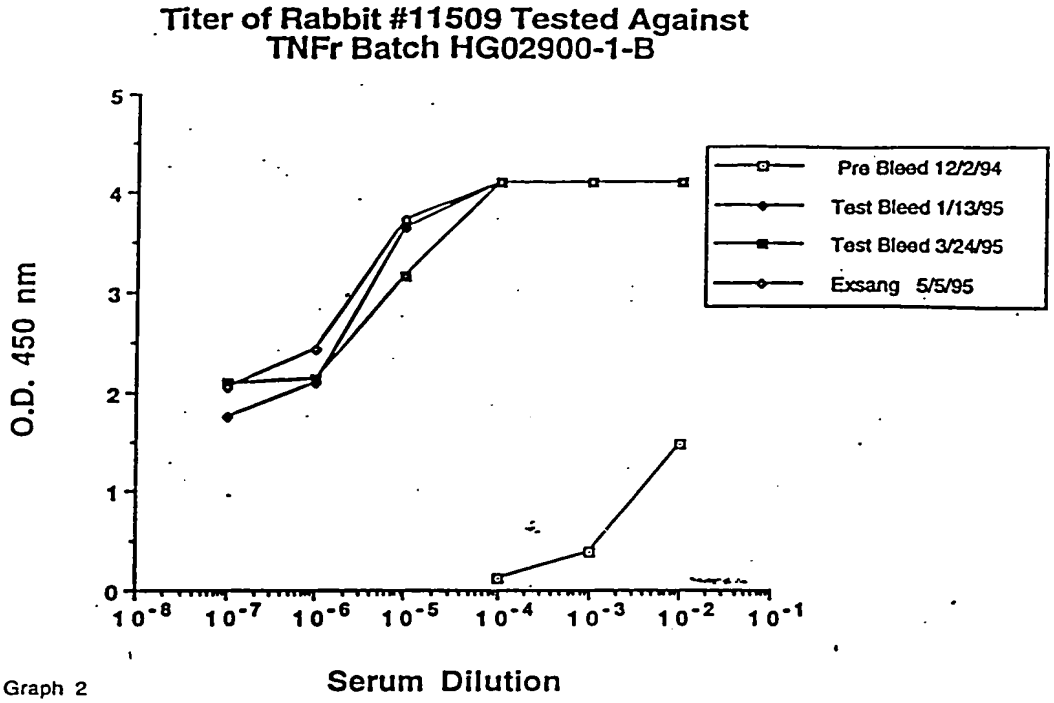


FIGURE 8


Titer of Rabbit #11509 Tested Against
TNFr Batch HG02900-1-B
O.D. 450 nm
Serum Dilution
Pre Bleed 12/2/94
Test Bleed 1/13/95
Test Bleed 3/24/95
Exsang 5/5/95
2900.01 Graph 2

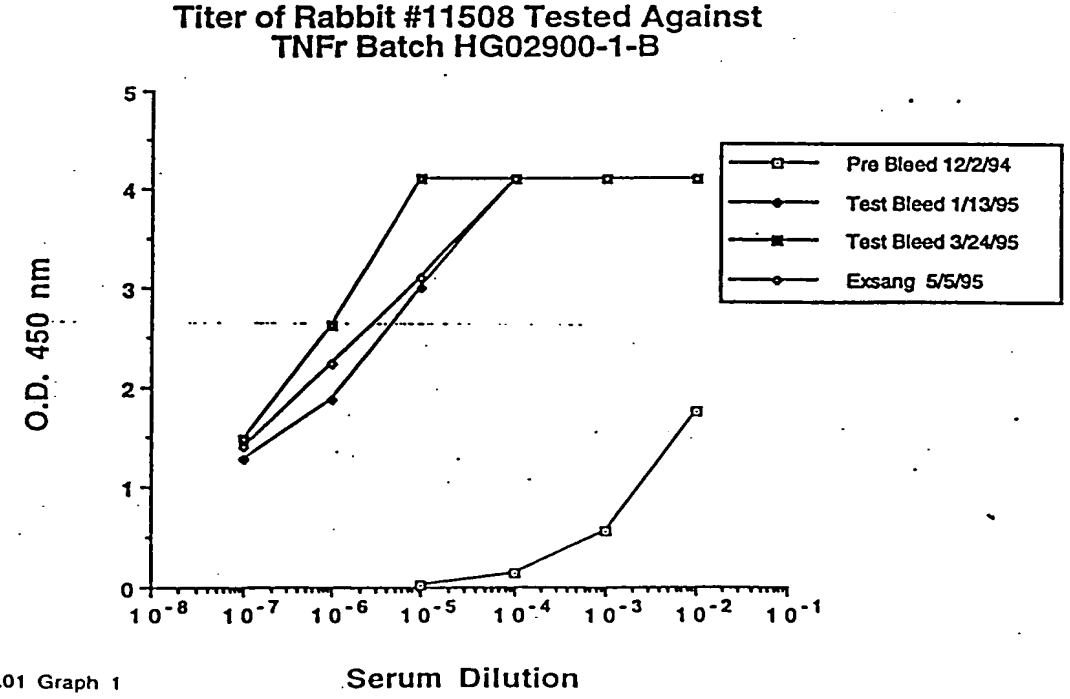

Titer of Rabbit #11508 Tested Against
TNFr Batch HG02900-1-B
O.D. 450 nm
Serum Dilution
Pre Bleed 12/2/94
Test Bleed 1/13/95
Test Bleed 3/24/95
Exsang 5/5/95
2900.01 Graph 1

FIGURE 9